

## (1) GENERAL INFORMATION:

(i) APPLICANT: Greenspan, Daniel S  
Takahara, Kazuhiko  
Hoffman, Guy G

10 (ii) TITLE OF INVENTION: Mammalian Tolloid-Like Protein

(iii) NUMBER OF SEQUENCES: 13

## (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Quarles & Brady  
(B) STREET: 1 South Pinckney Street  
(C) CITY: Madison  
(D) STATE: WI  
(E) COUNTRY: US  
(F) ZIP: 53703

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0,  
Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Berson, Bennett J  
(B) REGISTRATION NUMBER: 37094  
(C) REFERENCE/DOCKET NUMBER: 960296.93839

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 608-251-5000  
(B) TELEFAX: 608-251-9166

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide probe"

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGTCCAGAC CGGAGCGGGT GTGGCCCGAT GGGGTCATCC CGTTTGTGAT TGGAGGGAAT 60  
TTCACAGGCA GCCAGAGGGC AGTCTTCCGG CAGGCCATGA GACACTGGGA GAAGCATACC 120  
TGTGTCACCT TCTTGAGCG CACAGATGAG GACAGCTATA TTGTATTAC CTACCGACCC 180  
TGCGGGTGCT GCTCCTACGT GGGTCGCCGA GGTGGGGGCC CCCAGGCCAT CTCCATCGGC 240  
50 AAGAACTGTG ACAAGTTTGG CATCGTGGTC CATGAGCTGG GCCATGTCAT TGGCTTCTGG 300  
CACGAGACA CGCGGCCCGA CCGCGACCGC 330

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4771 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 611..3652  
(D) OTHER INFORMATION: /product= "murine mTll protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACACCCCTT TGCTCTCCGG GCAGTCGGGA GCTTCCCTAG CTTCGGCAGG CTTTAAAGGT 60  
CTGGCGGCGT AGAAATGCCT ATCCCCCACC CCCTTCCTCG GTCTCCCTT TCAGTTCAGA 120  
TGTGCTGATG TGCAGACCGG ATTCATCTTC CCCGAGCAGC GGCGGTGGCA GCGGCGGGCG 180  
CAGGCGGCTG CAGCTCGCTC TCGGCCGCGG GGTCTTGACA GCGGCGGGGG CGCGGCGCGG 240  
GAGCCGGAGC TCCGGTGGCA GCTGAGCCCG CCGTGCGCCT CTCGCCGCGG CCGGTCTGTA 300  
TCGCGGGAAG TTCGACCGCT GGAAGGACGA CCTAGACCGA GCCGGGTGG CTGCGGCTGC 360  
CCTGCGCCGA GCTCCTCACC TGCCTTCCGC CCACCCGCGG GCCCCCGGCC AAGTTCCCCA 420  
GCATCCGGGG GAGACAGGGA GACATTTGCC CTCTCTAGCG TCCTGAAGAC ATCCGCATGT 480  
CTCCGGACAC CTGAACATTC AGGTCTTTCC GAGGAGCTTC CCAGTCGGGA TAAGAACACT 540  
GTCCCTAGAG CCCCGCATAT CCACGCGGCC CTCCGGGTCT GGTCCCCTCC TTTTCCTCTA 600  
GGGGAGGAGG ATG GGT TTG CAA GCG CTC TCC CCG AGG ATG CTC CTG TGG 649  
Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp  
1 5 10  
TTG GTG GTC TCG GGT ATT GTT TTC TCC CGG GTG CTG TGG GTC TGC GCT 697  
Leu Val Val Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala  
15 20 25  
GGC CTC GAT TAT GAT TAC ACT TTT GAT GGG AAC GAA GAG GAC AAA ACG 745  
Gly Leu Asp Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr  
30 35 40 45  
GAG CCT ATA GAT TAC AAG GAC CCG TGC AAA GCT GCT GTG TTT TGG GGT 793  
Glu Pro Ile Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly  
50 55 60  
GAC ATC GCC TTA GAT GAT GAA GAC TTA AAT ATC TTC CAA ATA GAC AGG 841  
Asp Ile Ala Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg  
65 70 75  
ACA ATT GAC CTG ACC CAG AGC CCC TTT GGA AAA CTT GGA CAT ATT ACA 889  
Thr Ile Asp Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr  
80 85 90  
GGT GGC TTT GGA GAC CAT GGC ATG CCA AAG AAG CGA GGG GCA CTC TAC 937  
Gly Gly Phe Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr  
95 100 105

5	CAA Gln 110	CTT Leu	ATA Ile	GAG Glu	AGG Arg	ATC Ile 115	AGA Arg	AGA Arg	ATT Ile	GGC Gly	TCT Ser 120	GGC Gly	TTG Leu	GAG Glu	CAA Gln	AAT Asn 125	985
	AAC Asn	ACG Thr	ATG Met	AAG Lys	GGA Gly 130	AAA Lys	GCA Ala	CCT Pro	CCA Pro	AAA Lys 135	TTG Leu	TCA Ser	GAG Glu	CAA Gln	AGT Ser	GAG Glu 140	1033
	AAA Lys	AAT Asn	CGA Arg	GTT Val 145	CCC Pro	AGA Arg	GCT Ala	GCT Ala	ACC Thr 150	TCA Ser	AGA Arg	ACG Thr	GAA Glu	AGG Arg 155	ATA Ile	TGG Trp	1081
10	CCT Pro	GGG Gly	GGT Gly 160	GTC Val	ATT Ile	CCT Pro	TAT Tyr	GTC Val 165	ATA Ile	GGA Gly	GGA Gly	AAC Asn	TTT Phe 170	ACT Thr	GGC Gly	AGC Ser	1129
15	CAG Gln 175	AGA Arg	GCC Ala	ATG Met	TTC Phe	AAG Lys	CAG Gln 180	GCC Ala	ATG Met	AGA Arg	CAC His	TGG Trp 185	GAA Glu	AAG Lys	CAC His	ACC Thr	1177
	TGT Cys 190	GTG Val	ACG Thr	TTC Phe	ACT Thr	GAG Glu 195	AGA Arg	AGT Ser	GAT Asp	GAA Glu	GAA Glu 200	AGT Ser	TAT Tyr	ATT Ile	GTG Val	TTC Phe 205	1225
	ACC Thr	TAC Tyr	AGG Arg	CCT Pro	TGT Cys 210	GGA Gly	TGC Cys	TGC Cys	TCC Ser	TAT Tyr 215	GTT Val	GGT Gly	CGG Arg	CGG Arg	GGA Gly 220	AAT Asn	1273
20	GGC Gly	CCT Pro	CAG Gln	GCC Ala 225	ATC Ile	TCT Ser	ATT Ile	GGC Gly 230	AAG Lys	AAC Asn	TGT Cys	GAC Asp	AAG Lys	TTT Phe 235	GGA Gly	ATT Ile	1321
	GTT Val	GTT Val	CAT His 240	GAA Glu	CTG Leu	GGC Gly	CAC His	GTG Val 245	ATA Ile	GGC Gly	TTC Phe	TGG Trp 250	CAT His	GAA Glu	CAT His	ACC Thr	1369
	CGC Arg	CCA Pro 255	GAC Asp	CGA Arg	GAC Asp	AAC Asn	CAT His 260	GTC Val	ACC Thr	ATC Ile	ATT Ile 265	AGA Arg	GAG Glu	AAC Asn	ATC Ile	CAG Gln	1417
35	CCA Pro 270	GGT Gly	CAA Gln	GAG Glu	TAC Tyr 275	AAT Asn	TTT Phe	CTA Leu	AAG Lys	ATG Met	GAG Glu 280	CCT Pro	GGA Gly	GAA Glu	GTG Val	AAC Asn 285	1465
	TCT Ser	CTT Leu	GGG Gly	GAA Glu 290	AGA Arg	TAT Tyr	GAT Asp	TTT Phe	GAC Asp	AGT Ser 295	ATC Ile	ATG Met	CAC His	TAC Tyr	GCC Ala 300	AGG Arg	1513
	AAC Asn	ACC Thr	TTC Phe 305	TCA Ser	AGA Arg	GGG Gly	ATG Met	TTT Phe	TTA Leu 310	GAC Asp	ACA Thr	ATA Ile	CTC Leu	CCC Pro 315	TCC Ser	CGT Arg	1561
40	GAT Asp	GAT Asp	AAT Asn 320	GGC Gly	ATT Ile	CGT Arg	CCT Pro	GCA Ala 325	ATT Ile	GGT Gly	CAA Gln	CGG Arg	ACC Thr 330	CGG Arg	TTA Leu	AGC Ser	1609
45	AAA Lys	GGA Gly 335	GAC Asp	ATT Ile	GCA Ala	CAA Gln	GCA Ala 340	AGA Arg	AAG Lys	CTG Leu	TAT Tyr 345	CGA Arg	TGC Cys	CCA Pro	GCA Ala	TGT Cys	1657
	GGA Gly 350	GAA Glu	ACC Thr	CTG Leu	CAA Gln	GAA Glu 355	TCC Ser	AGT Ser	GGC Gly	AAC Asn	CTT Leu 360	TCT Ser	TCC Ser	CCA Pro	GGA Gly	TTC Phe 365	1705
	CCA Pro	AAT Asn	GGC Gly	TAC Tyr 370	CCT Pro	TCC Ser	TAC Tyr	ACA Thr	CAC His	TGC Cys 375	ATC Ile	TGG Trp	AGA Arg	GTG Val	TCT Ser 380	GTG Val	1753

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		ACC	CCG	GGA	GAA	AAG	ATT	GTC	TTG	AAT	TTT	ACC	ACA	ATG	GAC	CTT	TAC	1801
		Thr	Pro	Gly	Glu	Lys	Ile	Val	Leu	Asn	Phe	Thr	Thr	Met	Asp	Leu	Tyr	
					385					390					395			
5		AAA	AGT	AGT	TTG	TGC	TGG	TAT	GAT	TAC	ATT	GAA	GTA	AGA	GAT	GGT	TAC	1849
		Lys	Ser	Ser	Leu	Cys	Trp	Tyr	Asp	Tyr	Ile	Glu	Val	Arg	Asp	Gly	Tyr	
				400					405					410				
		TGG	AGG	AAG	TCA	CCT	CTC	CTT	GGT	AGA	TTC	TGT	GGG	GAC	AAA	GTG	GCT	1897
		Trp	Arg	Lys	Ser	Pro	Leu	Leu	Gly	Arg	Phe	Cys	Gly	Asp	Lys	Val	Ala	
				415				420					425					
10		GGA	GTT	CTT	ACA	TCT	ACG	GAC	AGC	AGA	ATG	TGG	ATT	GAG	TTT	CGT	AGC	1945
		Gly	Val	Leu	Thr	Ser	Thr	Asp	Ser	Arg	Met	Trp	Ile	Glu	Phe	Arg	Ser	
							435					440					445	
		AGC	AGT	AAC	TGG	GTA	GGA	AAA	GGG	TTT	GCA	GCT	GTC	TAT	GAA	GCG	ATT	1993
		Ser	Ser	Asn	Trp	Val	Gly	Lys	Gly	Phe	Ala	Ala	Val	Tyr	Glu	Ala	Ile	
15						450					455					460		
		TGT	GGA	GGG	GAG	ATA	AGG	AAA	AAC	GAA	GGG	CAG	ATT	CAG	TCT	CCC	AAT	2041
		Cys	Gly	Gly	Glu	Ile	Arg	Lys	Asn	Glu	Gly	Gln	Ile	Gln	Ser	Pro	Asn	
					465					470					475			
		TAC	CCC	GAT	GAC	TAC	CGA	CCA	ATG	AAG	GAG	TGT	GTA	TGG	AAA	ATA	ATG	2089
		Tyr	Pro	Asp	Asp	Tyr	Arg	Pro	Met	Lys	Glu	Cys	Val	Trp	Lys	Ile	Met	
				480					485					490				
		GTG	TCC	GAG	GGC	TAC	CAT	GTT	GGA	CTG	ACC	TTT	CAG	GCC	TTT	GAG	ATC	2137
		Val	Ser	Glu	Gly	Tyr	His	Val	Gly	Leu	Thr	Phe	Gln	Ala	Phe	Glu	Ile	
				495				500					505					
		GAA	AGA	CAT	GAC	AGC	TGT	GCC	TAT	GAC	CAC	CTA	GAA	GTT	CGA	GAT	GGA	2185
		Glu	Arg	His	Asp	Ser	Cys	Ala	Tyr	Asp	His	Leu	Glu	Val	Arg	Asp	Gly	
				510			515					520					525	
		GCC	AGT	GAG	AAC	AGC	CCT	TTG	ATA	GGA	CGG	TTC	TGT	GGT	TAT	GAC	AAA	2233
		Ala	Ser	Glu	Asn	Ser	Pro	Leu	Ile	Gly	Arg	Phe	Cys	Gly	Tyr	Asp	Lys	
						530					535						540	
		CCT	GAA	GAT	ATA	AGG	TCT	ACT	TCC	AAC	ACC	CTG	TGG	ATG	AAG	TTT	GTC	2281
		Pro	Glu	Asp	Ile	Arg	Ser	Thr	Ser	Asn	Thr	Leu	Trp	Met	Lys	Phe	Val	
					545					550					555			
		TCT	GAC	GGG	ACT	GTG	AAC	AAG	GCA	GGG	TTT	GCT	GCG	AAC	TTT	TTT	AAA	2329
35		Ser	Asp	Gly	Thr	Val	Asn	Lys	Ala	Gly	Phe	Ala	Ala	Asn	Phe	Phe	Lys	
				560					565					570				
		GAG	GAA	GAT	GAG	TGT	GCC	AAA	CCT	GAC	CGA	GGA	GGC	TGT	GAA	CAG	AGG	2377
		Glu	Glu	Asp	Glu	Cys	Ala	Lys	Pro	Asp	Arg	Gly	Gly	Cys	Glu	Gln	Arg	
				575				580					585					
		TGT	CTT	AAC	ACA	CTA	GGC	AGC	TAC	CAG	TGT	GCC	TGT	GAG	CCT	GGC	TAT	2425
40		Cys	Leu	Asn	Thr	Leu	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	
							595					600					605	
		GAA	CTG	GGG	CCA	GAC	AGA	AGA	AGC	TGT	GAA	GCT	GCT	TGC	GGA	GGA	CTT	2473
45		Glu	Leu	Gly	Pro	Asp	Arg	Arg	Ser	Cys	Glu	Ala	Ala	Cys	Gly	Gly	Leu	
						610					615					620		
		CTG	ACG	AAG	CTC	AAT	GGC	ACC	ATA	ACC	ACC	CCC	GGC	TGG	CCC	AAA	GAG	2521
		Leu	Thr	Lys	Leu	Asn	Gly	Thr	Ile	Thr	Thr	Pro	Gly	Trp	Pro	Lys	Glu	
					625					630					635			
		TAC	CCT	CCA	AAC	AAA	AAC	TGT	GTG	TGG	CAA	GTG	ATC	GCG	CCA	AGC	CAG	2569
50		Tyr	Pro	Pro	Asn	Lys	Asn	Cys	Val	Trp	Gln	Val	Ile	Ala	Pro	Ser	Gln	
				640					645					650				

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	TAC	AGA	ATC	TCT	GTG	AAG	TTT	GAG	TTT	TTT	GAA	TTG	GAA	GGC	AAT	GAA	2617
	Tyr	Arg	Ile	Ser	Val	Lys	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	
		655					660					665					
5	GTT	TGC	AAA	TAC	GAT	TAC	GTG	GAG	ATC	TGG	AGC	GGC	CCT	TCC	TCT	GAG	2665
	Val	Cys	Lys	Tyr	Asp	Tyr	Val	Glu	Ile	Trp	Ser	Gly	Pro	Ser	Ser	Glu	
		670				675					680					685	
	TCT	AAA	CTG	CAT	GGC	AAG	TTC	TGT	GGC	GCT	GAC	ATA	CCT	GAA	GTG	ATG	2713
	Ser	Lys	Leu	His	Gly	Lys	Phe	Cys	Gly	Ala	Asp	Ile	Pro	Glu	Val	Met	
					690					695					700		
10	ACT	TCC	CAT	TTC	AAC	AAC	ATG	AGG	ATT	GAA	TTC	AAG	TCA	GAC	AAC	ACT	2761
	Thr	Ser	His	Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	
				705					710					715			
	GTA	TCC	AAG	AAG	GGC	TTC	AAA	GCA	CAT	TTT	TTC	TCA	GAT	AAG	GAT	GAG	2809
15	Val	Ser	Lys	Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	
			720					725					730				
	TGT	TCA	AAG	GAT	AAT	GGT	GGC	TGT	CAG	CAT	GAG	TGT	GTC	AAC	ACG	ATG	2857
	Cys	Ser	Lys	Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	
		735					740					745					
20	GGA	AGT	TAC	ACG	TGT	CAG	TGC	CGG	AAT	GGA	TTC	GTG	TTG	CAT	GAG	AAC	2905
	Gly	Ser	Tyr	Thr	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Glu	Asn	
						755					760					765	
	AAG	CAT	GAT	TGC	AAG	GAA	GCC	GAG	TGT	GAA	CAG	AAG	ATA	CAC	AGC	CCA	2953
	Lys	His	Asp	Cys	Lys	Glu	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	
					770					775					780		
25	AGT	GGT	CTC	ATC	ACC	AGT	CCC	AAC	TGG	CCA	GAC	AAG	TAT	CCA	AGC	AGG	3001
	Ser	Gly	Leu	Ile	Thr	Ser	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	
				785					790					795			
	AAA	GAG	TGC	ACG	TGG	GTG	ATC	AGT	GCC	ATT	CCT	GGC	CAC	CGC	ATC	ACA	3049
30	Lys	Glu	Cys	Thr	Trp	Val	Ile	Ser	Ala	Ile	Pro	Gly	His	Arg	Ile	Thr	
			800					805					810				
	TTA	GCC	TTC	AAT	GAG	TTT	GAG	GTT	GAA	CAA	CAT	CAA	GAA	TGT	GCT	TAT	3097
	Leu	Ala	Phe	Asn	Glu	Phe	Glu	Val	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	
		815					820					825					
35	GAT	CAC	TTG	GAA	ATT	TTT	GAT	GGA	GAA	ACG	GAG	AAG	TCA	CCA	ATA	CTT	3145
	Asp	His	Leu	Glu	Ile	Phe	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	
		830				835					840					845	
	GGC	CGA	CTA	TGT	GGC	AGC	AAG	ATA	CCA	GAT	CCC	CTC	ATG	GCT	ACT	GGG	3193
	Gly	Arg	Leu	Cys	Gly	Ser	Lys	Ile	Pro	Asp	Pro	Leu	Met	Ala	Thr	Gly	
					850					855					860		
40	AAT	GAA	ATG	TTT	ATT	CGG	TTT	ATT	TCT	GAT	GCC	TCT	GTT	CAA	AGA	AAA	3241
	Asn	Glu	Met	Phe	Ile	Arg	Phe	Ile	Ser	Asp	Ala	Ser	Val	Gln	Arg	Lys	
				865					870					875			
	GGC	TTT	CAA	GCT	ACA	CAT	TCC	ACA	GAG	TGT	GGT	GGT	CGA	TTG	AAA	GCA	3289
45	Gly	Phe	Gln	Ala	Thr	His	Ser	Thr	Glu	Cys	Gly	Gly	Arg	Leu	Lys	Ala	
			880					885					890				
	GAG	TCA	AAG	CCT	AGA	GAC	CTG	TAC	TCC	CAT	GCT	CAG	TTT	GGT	GAT	AAT	3337
	Glu	Ser	Lys	Pro	Arg	Asp	Leu	Tyr	Ser	His	Ala	Gln	Phe	Gly	Asp	Asn	
		895					900					905					
50	AAC	TAC	CCA	GGA	CAA	CTG	GAC	TGT	GAA	TGG	TTG	TTG	GTG	TCA	GAA	CGA	3385
	Asn	Tyr	Pro	Gly	Gln	Leu	Asp	Cys	Glu	Trp	Leu	Leu	Val	Ser	Glu	Arg	
		910				915					920					925	

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	GGA TCT CGA CTT GAA TTG TCC TTC CAG ACA TTC GAA GTA GAA GAA GAA	3433
	Gly Ser Arg Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Glu	
	930 935 940	
5	GCT GAC TGT GGC TAT GAC TAT GTT GAA GTC TTT GAT GGT CTC AGT TCA	3481
	Ala Asp Cys Gly Tyr Asp Tyr Val Glu Val Phe Asp Gly Leu Ser Ser	
	945 950 955	
	AAA GCT GTG GGT CTT GGT AGA TTC TGT GGG TCA GGG CCA CCA GAA GAA	3529
	Lys Ala Val Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu	
	960 965 970	
10	ATC TAT TCA ATT GGA GAT GTG GCT TTG ATT CAT TTC CAC ACA GAT GAC	3577
	Ile Tyr Ser Ile Gly Asp Val Ala Leu Ile His Phe His Thr Asp Asp	
	975 980 985	
	ACT ATC AAC AAG AAA GGA TTT TAT ATA AGA TAT AAA AGT ATA AGA TAC	3625
	Thr Ile Asn Lys Lys Gly Phe Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr	
15	990 995 1000 1005	
	CCG GAA ACG ATG CAT GCC AAG AAC TAA TGCCGACCCT CCCTCAGAAC	3672
	Pro Glu Thr Met His Ala Lys Asn *	
	1010	
	AGAAAGGAAT GTGCATATGG AAAGAAGACA TTTTAAAAAT AGACAATATT AATACAATTG	3732
	TTTTATATAA TGAATTTGAG CAAAAGAAAC CTGCAAGATT AGAGTTATCT CTGAAGTGAA	3792
	AGAGAACTTT CCAGAAAACC TGATTGGCAT TGCAAGGATG TTTGAAAGTC ATGCTTGTTC	3852
	AAGGAAGATT AACAGCTTGA AATAGATGCT TCACATTTTG GACAGTTCAT TTAATGAGCT	3912
	GTGATTCTCT GGAGTGATTT CTTGACTACT TTTCCAAGAT CTGGGGACGT AGAAATGATG	3972
	GGACGGATCA TAGCTTGGA ACCCACTTCT TGGGTCTTAG CATGTTTGCT TAGACTCTGT	4032
	AGGTCAGACA CAGTGTA AAC CAAATTCATG TAAGGTGATG TGAATAGTG GTCTTTGGAA	4092
	GGTGGTTCAT CATTTAAATG TAGGTTTGTG CTTGTGTGTA TGTTACATA TGCAAGGTG	4152
	TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGCGTG TGTGTGTGTG TGCGTGTGTG	4212
	TGTGTGTGCA TGTGTGTGCA TGTGTGTTTG GAAACTGGAA TATTTTCATCT TCATTATTTT	4272
	CAAATGCAGG CCAGCTTAAC CTGTTCACAC AAATGATTTT GTGACCACTT CATTGTATCT	4332
30	GTATCTTGAG AAGTTTGAAA TATCTATAGT GTCTACAATG CAGTTAATCC CTAGATATCG	4392
	GATAATACCC AGTTCAC TAG TAAACTCATT TCTCTCTGGG GAAGTGCTGA ATAGTCTCCA	4452
	AATCAAGAA ACTCACCATG TCTTATAAAC CTTTAAGATA AAATTCCAAC GAGGTGTGTG	4512
	CAGCCATCTT CCAAATGACT GCCTGGATGT TTCTTAGTCC AGTTACTACT GCTGCTGCTA	4572
	TTGGTCTTTC TTTTATTGTT AATGTGTTGA TATGTTGTTA TTATTATGGT TATTATTATT	4632
35	GATGTTGTTA CTATATTTAA AAATGATGAG ATGAAGTGGA AGTAGAGTTT GGGAGAAATG	4692
	AAATCTCTCT TTTTGTTCCT CTCCTTGAAA TTCAGTTTCA AAAAATACAA TATTGGGTGG	4752
	CAAAAAAAAA AAAAAAAAAA	4771

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp Leu Val Val  
1 5 10 15  
Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala Gly Leu Asp  
20 25 30  
Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Pro Ile  
35 40 45  
Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala  
50 55 60  
Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp  
65 70 75 80  
Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr Gly Gly Phe  
85 90 95  
Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile  
100 105 110  
Glu Arg Ile Arg Arg Ile Gly Ser Gly Leu Glu Gln Asn Asn Thr Met  
115 120 125  
Lys Gly Lys Ala Pro Pro Lys Leu Ser Glu Gln Ser Glu Lys Asn Arg  
130 135 140  
Val Pro Arg Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly  
145 150 155 160  
Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala  
165 170 175  
Met Phe Lys Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr  
180 185 190  
Phe Thr Glu Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg  
195 200 205  
Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln  
210 215 220  
Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His  
225 230 235 240  
Glu Leu Gly His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp  
245 250 255  
Arg Asp Asn His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln  
260 265 270  
Glu Tyr Asn Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly  
275 280 285  
Glu Arg Tyr Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe  
290 295 300

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5

10

5

0

5

30

35

40

Ser	Arg	Gly	Met	Phe	Leu	Asp	Thr	Ile	Leu	Pro	Ser	Arg	Asp	Asp	Asn
305					310					315					320
Gly	Ile	Arg	Pro	Ala	Ile	Gly	Gln	Arg	Thr	Arg	Leu	Ser	Lys	Gly	Asp
				325					330					335	
Ile	Ala	Gln	Ala	Arg	Lys	Leu	Tyr	Arg	Cys	Pro	Ala	Cys	Gly	Glu	Thr
			340					345					350		
Leu	Gln	Glu	Ser	Ser	Gly	Asn	Leu	Ser	Ser	Pro	Gly	Phe	Pro	Asn	Gly
		355					360					365			
Tyr	Pro	Ser	Tyr	Thr	His	Cys	Ile	Trp	Arg	Val	Ser	Val	Thr	Pro	Gly
	370					375					380				
Glu	Lys	Ile	Val	Leu	Asn	Phe	Thr	Thr	Met	Asp	Leu	Tyr	Lys	Ser	Ser
385					390					395					400
Leu	Cys	Trp	Tyr	Asp	Tyr	Ile	Glu	Val	Arg	Asp	Gly	Tyr	Trp	Arg	Lys
				405					410					415	
Ser	Pro	Leu	Leu	Gly	Arg	Phe	Cys	Gly	Asp	Lys	Val	Ala	Gly	Val	Leu
			420					425					430		
Thr	Ser	Thr	Asp	Ser	Arg	Met	Trp	Ile	Glu	Phe	Arg	Ser	Ser	Ser	Asn
		435					440					445			
Trp	Val	Gly	Lys	Gly	Phe	Ala	Ala	Val	Tyr	Glu	Ala	Ile	Cys	Gly	Gly
	450					455					460				
Glu	Ile	Arg	Lys	Asn	Glu	Gly	Gln	Ile	Gln	Ser	Pro	Asn	Tyr	Pro	Asp
465					470					475					480
Asp	Tyr	Arg	Pro	Met	Lys	Glu	Cys	Val	Trp	Lys	Ile	Met	Val	Ser	Glu
				485					490					495	
Gly	Tyr	His	Val	Gly	Leu	Thr	Phe	Gln	Ala	Phe	Glu	Ile	Glu	Arg	His
			500					505					510		
Asp	Ser	Cys	Ala	Tyr	Asp	His	Leu	Glu	Val	Arg	Asp	Gly	Ala	Ser	Glu
		515					520					525			
Asn	Ser	Pro	Leu	Ile	Gly	Arg	Phe	Cys	Gly	Tyr	Asp	Lys	Pro	Glu	Asp
		530				535					540				
Ile	Arg	Ser	Thr	Ser	Asn	Thr	Leu	Trp	Met	Lys	Phe	Val	Ser	Asp	Gly
545					550					555					560
Thr	Val	Asn	Lys	Ala	Gly	Phe	Ala	Ala	Asn	Phe	Phe	Lys	Glu	Glu	Asp
				565					570					575	
Glu	Cys	Ala	Lys	Pro	Asp	Arg	Gly	Gly	Cys	Glu	Gln	Arg	Cys	Leu	Asn
			580					585					590		
Thr	Leu	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Glu	Leu	Gly
		595					600					605			
Pro	Asp	Arg	Arg	Ser	Cys	Glu	Ala	Ala	Cys	Gly	Gly	Leu	Leu	Thr	Lys
	610					615					620				
Leu	Asn	Gly	Thr	Ile	Thr	Thr	Pro	Gly	Trp	Pro	Lys	Glu	Tyr	Pro	Pro
625					630					635					640
Asn	Lys	Asn	Cys	Val	Trp	Gln	Val	Ile	Ala	Pro	Ser	Gln	Tyr	Arg	Ile
				645					650					655	



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	Ser	Val	Lys	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys
				660					665					670		
	Tyr	Asp	Tyr	Val	Glu	Ile	Trp	Ser	Gly	Pro	Ser	Ser	Glu	Ser	Lys	Leu
			675					680					685			
5	His	Gly	Lys	Phe	Cys	Gly	Ala	Asp	Ile	Pro	Glu	Val	Met	Thr	Ser	His
		690					695					700				
	Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys
	705					710					715					720
10	Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	Cys	Ser	Lys
					725					730					735	
	Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr
				740					745					750		
	Thr	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Glu	Asn	Lys	His	Asp
				755				760					765			
15	Cys	Lys	Glu	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	Ser	Gly	Leu
		770					775					780				
	Ile	Thr	Ser	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	Lys	Glu	Cys
	785					790					795					800
20	Thr	Trp	Val	Ile	Ser	Ala	Ile	Pro	Gly	His	Arg	Ile	Thr	Leu	Ala	Phe
					805					810					815	
	Asn	Glu	Phe	Glu	Val	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	Asp	His	Leu
				820					825					830		
	Glu	Ile	Phe	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	Gly	Arg	Leu
			835					840					845			
25	Cys	Gly	Ser	Lys	Ile	Pro	Asp	Pro	Leu	Met	Ala	Thr	Gly	Asn	Glu	Met
		850					855					860				
	Phe	Ile	Arg	Phe	Ile	Ser	Asp	Ala	Ser	Val	Gln	Arg	Lys	Gly	Phe	Gln
	865					870					875					880
30	Ala	Thr	His	Ser	Thr	Glu	Cys	Gly	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Lys
					885					890					895	
	Pro	Arg	Asp	Leu	Tyr	Ser	His	Ala	Gln	Phe	Gly	Asp	Asn	Asn	Tyr	Pro
				900					905					910		
	Gly	Gln	Leu	Asp	Cys	Glu	Trp	Leu	Leu	Val	Ser	Glu	Arg	Gly	Ser	Arg
			915					920					925			
35	Leu	Glu	Leu	Ser	Phe	Gln	Thr	Phe	Glu	Val	Glu	Glu	Glu	Ala	Asp	Cys
		930					935					940				
	Gly	Tyr	Asp	Tyr	Val	Glu	Val	Phe	Asp	Gly	Leu	Ser	Ser	Lys	Ala	Val
	945					950					955					960
40	Gly	Leu	Gly	Arg	Phe	Cys	Gly	Ser	Gly	Pro	Pro	Glu	Glu	Ile	Tyr	Ser
					965					970					975	
	Ile	Gly	Asp	Val	Ala	Leu	Ile	His	Phe	His	Thr	Asp	Asp	Thr	Ile	Asn
				980					985					990		
	Lys	Lys	Gly	Phe	Tyr	Ile	Arg	Tyr	Lys	Ser	Ile	Arg	Tyr	Pro	Glu	Thr
			995					1000					1005			

Met His Ala Lys Asn \*  
1010

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3919 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 648..3689  
(D) OTHER INFORMATION: /product= "human mT11 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTCACACTTT TGCTCTCTTG CAGTCAGTTG CTTTGCTGGC TTCTGCAGGC TTTTAAGGTC 60  
TCGCGGCGTA GAAATGCCTG GCCCCACCC CCTTCCTCGG TCTCCCCTTT CAATTCAGAT 120  
GTGCTGATGT GCAGACCGGA TTCATCTTCT CGGAGCTGCG GCGGCGGCTT TGGGCTCAGG 180  
CGGCGGCGGC TCGCGCTCGG CCGCGGAGTC CTGGCAGCAG CGGGGACGCG GCGCGGGAGT 240  
CCGAGCTCTG GTGGCAGCTG AGCCCGCGGG GCGCCGCTCG CCGAGCCGCG GCCGCGGGAA 300  
GTTCCGCAGC CAGAAGGACG ACCTGGCAGG CTGCGAGCGC CAGCGCCGCC AGAGCCGAGT 360  
TTGCCTGCGC CCTCCCCGCC TCCGAGTGCA GAGTTCCTTA CCTGCCCTCC GCCCACCCTG 420  
GGGCCCCCTAG CCAACTTCTC CCTGCGACTG GGGGTAACAG GCAGTGCTTG CCCTCTCTAC 480  
TGTCCTGGCG GCATCCACAT GTTTCGGAC ACCTGAGCAC CCCGGTCCCG CCGAGGAGCC 540  
TCCGGGTGGG GAGAAGAGCA CCGGTGCCCC TAGCCCCGCA CATCAGCGCG GACCGCGGCT 600  
GCCTAACCTC TGGGTCCCGT CCCCTCCTTT TCCTCCGGGG GAGGAGG ATG GGG TTG 656  
Met Gly Leu  
1015  
GGA ACG CTT TCC CCG AGG ATG CTC GTG TGG CTG GTG GCC TCG GGG ATT 704  
Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala Ser Gly Ile  
1020 1025 1030  
GTT TTC TAC GGG GAG CTA TGG GTC TGC GCT GGC CTC GAT TAT GAT TAC 752  
Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp Tyr Asp Tyr  
1035 1040 1045  
ACT TTT GAT GGG AAC GAA GAG GAT AAA ACA GAG ACT ATA GAT TAC AAG 800  
Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Ile Thr Ile Asp Tyr Lys  
1050 1055 1060 1065  
GAC CCG TGT AAA GCC GCT GTA TTT TGG GGC GAT ATT GCC TTA GAT GAT 848  
Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala Leu Asp Asp  
1070 1075 1080

	GAA Glu	GAC Asp	TTA Leu	AAT Asn 1085	ATC Ile	TTT Phe	CAA Gln	ATA Ile 1090	GAT Asp	AGG Arg	ACA Thr	ATT Ile	GAC Asp 1095	CTT Leu	ACG Thr	CAG Gln	896
5	AAC Asn	CCC Pro	TTT Phe 1100	GGA Gly	AAC Asn	CTT Leu	GGA Gly 1105	CAT His 1105	ACC Thr	ACA Thr	GGT Gly	GGA Gly	CTT Leu 1110	GGA Gly	GAC Asp	CAT His	944
	GCT Ala	ATG Met 1115	TCA Ser	AAG Lys	AAG Lys	CGA Arg	GGG Gly 1120	GCC Ala	CTC Leu	TAC Tyr	CAA Gln	CTT Leu 1125	ATA Ile	GAC Asp	AGG Arg	ATA Ile	992
10	AGA Arg 1130	AGA Arg	ATT Ile	GGC Gly	TTT Phe 1135	GGC Leu	TTG Glu	GAG Gln	CAA Asn 1140	AAC Asn	AAC Thr	ACA Val	GTT Val	AAG Lys	GGA Gly	AAA Lys 1145	1040
15	GTA Val	CCT Pro	CTA Leu	CAA Gln 1150	TTC Phe	TCA Ser	GGG Gly	CAA Gln	AAT Asn 1155	GAG Glu	AAA Lys	AAT Asn	CGA Arg	GTT Val	CCC Pro	AGA Arg 1160	1088
	GCC Ala	GCT Ala	ACA Thr 1165	TCA Ser	AGA Arg	ACG Thr	GAA Glu	AGA Arg 1170	ATA Ile	TGG Trp	CCT Pro	GGA Gly	GGC Gly	GTT Val 1175	ATT Ile	CCT Pro	1136
20	TAT Tyr	GTT Val	ATA Ile 1180	GGA Gly	GGA Gly	AAC Asn	TTC Phe	ACT Thr 1185	GGC Gly	AGC Ser	CAG Gln	AGA Arg	GCC Ala 1190	ATG Met	TTC Phe	AAG Lys	1184
	CAG Gln	GCC Ala	ATG Met 1195	AGG Arg	CAC His	TGG Trp	GAA Glu 1200	AAG Lys	CAC His	ACA Thr	TGT Cys	GTG Val 1205	ACT Thr	TTC Phe	ATA Ile	GAA Glu	1232
25	AGA Arg 1210	AGT Ser	GAT Asp	GAA Glu	GAG Glu 1215	AGT Ser	TAC Tyr	ATT Ile	GTA Val	TTC Phe 1220	ACC Thr	TAT Tyr	AGG Arg	CCT Pro	TGT Cys	GGA Gly 1225	1280
	TGC Cys	TGC Cys	TCC Ser	TAT Tyr 1230	GTA Val	GGT Gly	CGG Arg	CGA Arg	GGA Gly	AAT Asn 1235	GGA Gly	CCT Pro	CAG Gln	GCA Ala	ATC Ile 1240	TCT Ser	1328
	ATC Ile	GGC Gly	AAG Lys 1245	AAC Asn	TGT Cys	GAT Asp	AAA Lys	TTT Phe	GGG Gly 1250	ATT Ile	GTT Val	GTT Val	CAT His 1255	GAA Glu	TTG Leu	GGT Gly	1376
35	CAT His	GTG Val	ATA Ile 1260	GGC Gly	TTT Phe	TGG Trp	CAT His	GAA Glu 1265	CAC His	ACA Thr	AGA Arg	CCA Pro	GAT Asp 1270	CGA Arg	GAT Asp	AAC Asn	1424
	CAC His	GTA Val	ACT Thr 1275	ATC Ile	ATA Ile	AGA Arg	GAA Glu 1280	AAC Asn	ATC Ile	CAG Gln	CCA Pro	GGT Gly 1285	CAA Gln	GAG Glu	TAC Tyr	AAT Asn	1472
40	TTT Phe 1290	CTG Leu	AAG Lys	ATG Met	GAG Glu 1295	CCT Pro	GGA Gly	GAA Glu	GTA Val	AAC Asn 1300	TCA Ser	CTT Leu	GGA Gly	GAA Glu	AGA Arg	TAT Tyr 1305	1520
45	GAT Asp	TTC Phe	GAC Asp	AGT Ser 1310	ATC Ile	ATG Met	CAC His	TAT Tyr	GCC Ala	AGG Arg 1315	AAC Asn	ACC Thr	TTC Phe	TCA Ser	AGG Arg	GGG Gly	1568
	ATG Met	TTT Phe	CTG Leu 1325	GAT Asp	ACC Thr	ATT Ile	CTC Leu	CCC Pro	TCC Ser 1330	CGT Arg	GAT Asp	GAT Asp	AAT Asn	GGC Gly 1335	ATA Ile	CGT Arg	1616
50	CCT Pro	GCA Ala	ATT Ile 1340	GGT Gly	CAG Gln	CGA Arg	ACC Thr	CGT Arg 1345	CTA Leu	AGC Ser	AAA Lys	GGA Gly	GAT Asp 1350	ATC Ile	GCA Ala	CAG Gln	1664

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	GCA AGA AAG CTG TAT AGA TGT CCA GCA TGT GGA GAA ACT CTA CAA GAA	1712
	Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys Gly Glu Thr Leu Gln Glu	
	1355 1360 1365	
5	TCC AAT GGC AAC CTT TCC TCT CCA GGA TTT CCC AAT GGC TAC CCT TCT	1760
	Ser Asn Gly Asn Leu Ser Ser Pro Gly Phe Pro Asn Gly Tyr Pro Ser	
	1370 1375 1380 1385	
	TAC ACA CAC TGC ATC TGG AGA GTT TCT GTG ACC CCA GGG GAG AAG ATT	1808
	Tyr Thr His Cys Ile Trp Arg Val Ser Val Thr Pro Gly Glu Lys Ile	
	1390 1395 1400	
10	GTT TTA AAT TTT ACA ACG ATG GAT CTA TAC AAG AGT AGT TTG TGC TGG	1856
	Val Leu Asn Phe Thr Thr Met Asp Leu Tyr Lys Ser Ser Leu Cys Trp	
	1405 1410 1415	
	TAT GAC TAT ATT GAA GTA AGA GAC GGG TAC TGG AGA AAA TCA CCT CTC	1904
	Tyr Asp Tyr Ile Glu Val Arg Asp Gly Tyr Trp Arg Lys Ser Pro Leu	
	1420 1425 1430	
15	CTT GGT AGA TTC TGT GGG GAC AAA TTG CCT GAA GTT CTT ACT TCT ACA	1952
	Leu Gly Arg Phe Cys Gly Asp Lys Leu Pro Glu Val Leu Thr Ser Thr	
	1435 1440 1445	
20	GAC AGC AGA ATG TGG ATT GAG TTT CGT AGC AGC AGT AAT TGG GTA GGA	2000
	Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn Trp Val Gly	
	1450 1455 1460 1465	
	AAA GGC TTT GCA GCT GTC TAT GAA GCG ATC TGT GGA GGT GAG ATA CGT	2048
	Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly Glu Ile Arg	
	1470 1475 1480	
25	AAA AAT GAA GGA CAG ATT CAG TCT CCC AAT TAT CCT GAT GAC TAT CGC	2096
	Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp Asp Tyr Arg	
	1485 1490 1495	
30	CCG ATG AAA GAA TGT GTG TGG AAA ATA ACA GTG TCT GAG AGC TAC CAC	2144
	Pro Met Lys Glu Cys Val Trp Lys Ile Thr Val Ser Glu Ser Tyr His	
	1500 1505 1510	
	GTC GGG CTG ACC TTT CAG TCC TTT GAG ATT GAA AGA CAT GAC AAT TGT	2192
	Val Gly Leu Thr Phe Gln Ser Phe Glu Ile Glu Arg His Asp Asn Cys	
	1515 1520 1525	
35	GCT TAT GAC TAC CTG GAA GTT AGA GAT GGA ACC AGT GAA AAT AGC CCT	2240
	Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly Thr Ser Glu Asn Ser Pro	
	1530 1535 1540 1545	
	TTG ATA GGG CGT TTC TGT GGT TAT GAC AAA CCT GAA GAC ATA AGA TCT	2288
	Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp Ile Arg Ser	
	1550 1555 1560	
40	ACC TCC AAT ACT TTG TGG ATG AAG TTT GTT TCT GAC GGA ACT GTG AAC	2336
	Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly Thr Val Asn	
	1565 1570 1575	
45	AAA GCA GGG TTT GCT GCT AAC TTT TTT AAA GAG GAA GAT GAG TGT GCC	2384
	Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp Glu Cys Ala	
	1580 1585 1590	
	AAA CCT GAC CGT GGA GGC TGT GAG CAG CGA TGT CTG AAC ACT CTG GGC	2432
	Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn Thr Leu Gly	
	1595 1600 1605	
50	AGT TAC CAG TGT GCC TGT GAG CCT GGC TAT GAG CTG GGC CCA GAC AGA	2480
	Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly Pro Asp Arg	
	1610 1615 1620 1625	

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	AGG AGC TGT GAA GCT GCT TGT GGT GGA CTT CTT ACC AAA CTT AAC GGC	2528
	Arg Ser Cys Glu Ala Ala Cys Gly Gly Leu Leu Thr Lys Leu Asn Gly	
	1630 1635 1640	
5	ACC ATA ACC ACC CCT GGC TGG CCC AAG GAG TAC CCT CCT AAT AAG AAC	2576
	Thr Ile Thr Thr Pro Gly Trp Pro Lys Glu Tyr Pro Pro Asn Lys Asn	
	1645 1650 1655	
	TGT GTG TGG CAA GTG GTT GCA CCA ACC CAG TAC AGA ATT TCT GTG AAG	2624
	Cys Val Trp Gln Val Val Ala Pro Thr Gln Tyr Arg Ile Ser Val Lys	
	1660 1665 1670	
10	TTT GAG TTT TTT GAA TTG GAA GGC AAT GAA GTT TGC AAA TAT GAT TAT	2672
	Phe Glu Phe Phe Glu Leu Glu Gly Asn Glu Val Cys Lys Tyr Asp Tyr	
	1675 1680 1685	
	GTG GAG ATC TGG AGT GGT CTT TCC TCT GAG TCT AAA CTG CAT GGC AAA	2720
	Val Glu Ile Trp Ser Gly Leu Ser Ser Glu Ser Lys Leu His Gly Lys	
15	1690 1695 1700 1705	
	TTC TGT GGC GCT GAA GTG CCT GAA GTG ATC ACA TCC CAG TTC AAC AAT	2768
	Phe Cys Gly Ala Glu Val Pro Glu Val Ile Thr Ser Gln Phe Asn Asn	
	1710 1715 1720	
20	ATG AGA ATT GAA TTC AAA TCT GAC AAT ACT GTA TCC AAG AAG GGC TTC	2816
	Met Arg Ile Glu Phe Lys Ser Asp Asn Thr Val Ser Lys Lys Gly Phe	
	1725 1730 1735	
	AAA GCA CAT TTT TTC TCA GAC AAA GAT GAA TGC TCT AAG GAT AAT GGT	2864
	Lys Ala His Phe Phe Ser Asp Lys Asp Glu Cys Ser Lys Asp Asn Gly	
	1740 1745 1750	
25	GGA TGT CAG CAC GAA TGT GTC AAC ACG ATG GGG AGC TAC ATG TGT CAA	2912
	Gly Cys Gln His Glu Cys Val Asn Thr Met Gly Ser Tyr Met Cys Gln	
	1755 1760 1765	
	TGC CGT AAT GGA TTT GTG CTA CAT GAC AAT AAA CAT GAT TGC AAG GAA	2960
	Cys Arg Asn Gly Phe Val Leu His Asp Asn Lys His Asp Cys Lys Glu	
	1770 1775 1780 1785	
	GCT GAG TGT GAA CAG AAG ATC CAC AGT CCA AGT GGC CTC ATC ACC AGT	3008
	Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu Ile Thr Ser	
	1790 1795 1800	
35	CCC AAC TGG CCA GAC AAG TAC CCA AGC AGG AAA GAA TGC ACT TGG GAA	3056
	Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys Thr Trp Glu	
	1805 1810 1815	
	ATC AGC GCC ACT CCC GGC CAC CGA ATC AAA TTA GCC TTT AGT GAA TTT	3104
	Ile Ser Ala Thr Pro Gly His Arg Ile Lys Leu Ala Phe Ser Glu Phe	
	1820 1825 1830	
40	GAG ATT GAG CAG CAT CAA GAA TGT GCT TAT GAC CAC TTA GAA GTA TTT	3152
	Glu Ile Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu Glu Val Phe	
	1835 1840 1845	
	GAT GGA GAA ACA GAA AAG TCA CCG ATT CTT GGA CGA CTA TGT GGC AAC	3200
	Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu Cys Gly Asn	
45	1850 1855 1860 1865	
	AAG ATA CCA GAT CCC CTT GTG GCT ACT GGA AAT AAA ATG TTT GTT CGG	3248
	Lys Ile Pro Asp Pro Leu Val Ala Thr Gly Asn Lys Met Phe Val Arg	
	1870 1875 1880	
50	TTT GTT TCT GAT GCA TCT GTT CAA AGA AAA GGC TTT CAA GCC ACA CAT	3296
	Phe Val Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln Ala Thr His	
	1885 1890 1895	

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5 TCT ACA GAG TGT GGC GGA CGA TTG AAA GCA GAA TCA AAA CCA AGA GAT 3344  
 Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys Pro Arg Asp  
 1900 1905 1910

CTG TAC TCA CAT GCT CAG TTT GGT GAT AAC AAC TAC CCA GGA CAG GTT 3392  
 Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro Gly Gln Val  
 1915 1920 1925

10 GAC TGT GAA TGG CTA TTA GTA TCA GAA CGG GGC TCT CGA CTT GAA TTA 3440  
 Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg Leu Glu Leu  
 1930 1935 1940 1945

TCC TTC CAG ACA TTT GAA GTG GAG GAA GAA GCA GAC TGT GGC TAT GAC 3488  
 Ser Phe Gln Thr Phe Glu Val Glu Glu Glu Ala Asp Cys Gly Tyr Asp  
 1950 1955 1960

15 TAT GTG GAG CTC TTT GAT GGT CTT GAT TCA ACA GCT GTG GGG CTT GGT 3536  
 Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val Gly Leu Gly  
 1965 1970 1975

CGA TTC TGT GGA TCC GGG CCA CCA GAA GAG ATT TAT TCA ATT GGA GAT 3584  
 Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser Ile Gly Asp  
 1980 1985 1990

TCA GTT TTA ATT CAT TTC CAC ACT GAT GAC ACA ATC AAC AAG AAG GGA 3632  
 Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn Lys Lys Gly  
 1995 2000 2005

TTT CAT ATA AGA TAC AAA AGC ATA AGA TAT CCA GAT ACC ACA CAT ACC 3680  
 Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr  
 2010 2015 2020 2025

AAA AAA TAA CACCAAACC TCTGTCAGAA CACAAAGGAA TGTGCATAAT 3729  
 Lys Lys \*

GGAGAGAAGA CATATTTTTT TTAAACTGA AGATATTGGC ACAAATGTTT TATACAAAGA 3789

GTTTGAACAA AAAATCCCTG TAAGACCAGA ATTATCTTTG TACTAAAAGA GAAGTTTCCA 3849

30 GCAAAACCCCT CATCAGCATT ACAAGGATAT TTGAACTCCA TGCTTGATGG TATTAATAAA 3909

GCTGGTGAAA 3919

(2) INFORMATION FOR SEQ ID NO:5:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1014 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

40 Met Gly Leu Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala  
 1 5 10 15

Ser Gly Ile Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly/Leu Asp  
 20 25 30

Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile  
 35 40 45

45 Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala  
 50 55 60

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	Leu	Asp	Asp	Glu	Asp	Leu	Asn	Ile	Phe	Gln	Ile	Asp	Arg	Thr	Ile	Asp	
	65					70					75					80	
	Leu	Thr	Gln	Asn	Pro	Phe	Gly	Asn	Leu	Gly	His	Thr	Thr	Gly	Gly	Leu	
					85					90					95		
5	Gly	Asp	His	Ala	Met	Ser	Lys	Lys	Arg	Gly	Ala	Leu	Tyr	Gln	Leu	Ile	
				100					105					110			
	Asp	Arg	Ile	Arg	Arg	Ile	Gly	Phe	Gly	Leu	Glu	Gln	Asn	Asn	Thr	Val	
			115					120					125				
10	Lys	Gly	Lys	Val	Pro	Leu	Gln	Phe	Ser	Gly	Gln	Asn	Glu	Lys	Asn	Arg	
		130					135					140					
	Val	Pro	Arg	Ala	Ala	Thr	Ser	Arg	Thr	Glu	Arg	Ile	Trp	Pro	Gly	Gly	
		145				150					155					160	
	Val	Ile	Pro	Tyr	Val	Ile	Gly	Gly	Asn	Phe	Thr	Gly	Ser	Gln	Arg	Ala	
					165					170					175		
15	Met	Phe	Lys	Gln	Ala	Met	Arg	His	Trp	Glu	Lys	His	Thr	Cys	Val	Thr	
				180					185					190			
	Phe	Ile	Glu	Arg	Ser	Asp	Glu	Glu	Ser	Tyr	Ile	Val	Phe	Thr	Tyr	Arg	
			195					200					205				
20	Pro	Cys	Gly	Cys	Cys	Ser	Tyr	Val	Gly	Arg	Arg	Gly	Asn	Gly	Pro	Gln	
		210					215					220					
	Ala	Ile	Ser	Ile	Gly	Lys	Asn	Cys	Asp	Lys	Phe	Gly	Ile	Val	Val	His	
		225				230					235					240	
	Glu	Leu	Gly	His	Val	Ile	Gly	Phe	Trp	His	Glu	His	Thr	Arg	Pro	Asp	
				245						250					255		
25	Arg	Asp	Asn	His	Val	Thr	Ile	Ile	Arg	Glu	Asn	Ile	Gln	Pro	Gly	Gln	
				260					265					270			
	Glu	Tyr	Asn	Phe	Leu	Lys	Met	Glu	Pro	Gly	Glu	Val	Asn	Ser	Leu	Gly	
			275					280					285				
30	Glu	Arg	Tyr	Asp	Phe	Asp	Ser	Ile	Met	His	Tyr	Ala	Arg	Asn	Thr	Phe	
			290				295					300					
	Ser	Arg	Gly	Met	Phe	Leu	Asp	Thr	Ile	Leu	Pro	Ser	Arg	Asp	Asp	Asn	
		305				310					315					320	
	Gly	Ile	Arg	Pro	Ala	Ile	Gly	Gln	Arg	Thr	Arg	Leu	Ser	Lys	Gly	Asp	
					325					330					335		
35	Ile	Ala	Gln	Ala	Arg	Lys	Leu	Tyr	Arg	Cys	Pro	Ala	Cys	Gly	Glu	Thr	
				340					345					350			
	Leu	Gln	Glu	Ser	Asn	Gly	Asn	Leu	Ser	Ser	Pro	Gly	Phe	Pro	Asn	Gly	
			355					360					365				
40	Tyr	Pro	Ser	Tyr	Thr	His	Cys	Ile	Trp	Arg	Val	Ser	Val	Thr	Pro	Gly	
		370					375					380					
	Glu	Lys	Ile	Val	Leu	Asn	Phe	Thr	Thr	Met	Asp	Leu	Tyr	Lys	Ser	Ser	
		385				390					395					400	
	Leu	Cys	Trp	Tyr	Asp	Tyr	Ile	Glu	Val	Arg	Asp	Gly	Tyr	Trp	Arg	Lys	
				405						410					415		

Ser	Pro	Leu	Leu	Gly	Arg	Phe	Cys	Gly	Asp	Lys	Leu	Pro	Glu	Val	Leu
			420					425					430		
Thr	Ser	Thr	Asp	Ser	Arg	Met	Trp	Ile	Glu	Phe	Arg	Ser	Ser	Ser	Asn
		435					440					445			
Trp	Val	Gly	Lys	Gly	Phe	Ala	Ala	Val	Tyr	Glu	Ala	Ile	Cys	Gly	Gly
	450					455					460				
Glu	Ile	Arg	Lys	Asn	Glu	Gly	Gln	Ile	Gln	Ser	Pro	Asn	Tyr	Pro	Asp
465				470						475					480
Asp	Tyr	Arg	Pro	Met	Lys	Glu	Cys	Val	Trp	Lys	Ile	Thr	Val	Ser	Glu
				485					490					495	
Ser	Tyr	His	Val	Gly	Leu	Thr	Phe	Gln	Ser	Phe	Glu	Ile	Glu	Arg	His
			500					505					510		
Asp	Asn	Cys	Ala	Tyr	Asp	Tyr	Leu	Glu	Val	Arg	Asp	Gly	Thr	Ser	Glu
		515					520					525			
Asn	Ser	Pro	Leu	Ile	Gly	Arg	Phe	Cys	Gly	Tyr	Asp	Lys	Pro	Glu	Asp
	530					535					540				
Ile	Arg	Ser	Thr	Ser	Asn	Thr	Leu	Trp	Met	Lys	Phe	Val	Ser	Asp	Gly
545					550					555					560
Thr	Val	Asn	Lys	Ala	Gly	Phe	Ala	Ala	Asn	Phe	Phe	Lys	Glu	Glu	Asp
				565					570					575	
Glu	Cys	Ala	Lys	Pro	Asp	Arg	Gly	Gly	Cys	Glu	Gln	Arg	Cys	Leu	Asn
			580					585					590		
Thr	Leu	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Glu	Leu	Gly
		595					600					605			
Pro	Asp	Arg	Arg	Ser	Cys	Glu	Ala	Ala	Cys	Gly	Gly	Leu	Leu	Thr	Lys
	610					615					620				
Leu	Asn	Gly	Thr	Ile	Thr	Thr	Pro	Gly	Trp	Pro	Lys	Glu	Tyr	Pro	Pro
625				630						635					640
Asn	Lys	Asn	Cys	Val	Trp	Gln	Val	Val	Ala	Pro	Thr	Gln	Tyr	Arg	Ile
				645					650					655	
Ser	Val	Lys	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys
			660					665					670		
Tyr	Asp	Tyr	Val	Glu	Ile	Trp	Ser	Gly	Leu	Ser	Ser	Glu	Ser	Lys	Leu
		675					680					685			
His	Gly	Lys	Phe	Cys	Gly	Ala	Glu	Val	Pro	Glu	Val	Ile	Thr	Ser	Gln
	690					695					700				
Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys
705					710					715					720
Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	Cys	Ser	Lys
				725					730					735	
Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr
			740					745					750		
Met	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Asp	Asn	Lys	His	Asp
		755					760					765			



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Cys Lys Glu Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu  
770 775 780

Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys  
785 790 795 800

5 Thr Trp Glu Ile Ser Ala Thr Pro Gly His Arg Ile Lys Leu Ala Phe  
805 810 815

Ser Glu Phe Glu Ile Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu  
820 825 830

10 Glu Val Phe Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu  
835 840 845

Cys Gly Asn Lys Ile Pro Asp Pro Leu Val Ala Thr Gly Asn Lys Met  
850 855 860

Phe Val Arg Phe Val Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln  
865 870 875 880

5 Ala Thr His Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys  
885 890 895

Pro Arg Asp Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro  
900 905 910

Gly Gln Val Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg  
915 920 925

Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Glu Ala Asp Cys  
930 935 940

Gly Tyr Asp Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val  
945 950 955 960

25 Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser  
965 970 975

Ile Gly Asp Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn  
980 985 990

30 Lys Lys Gly Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr  
995 1000 1005

Thr His Thr Lys Lys \*  
1010

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCAGCTTAAC CTGTTACAC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACTCTACTT CCACTTCATC

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGAACAGA AAGGAATGTG

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACCACTATT CCATCACC

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTTGCACTC AGTTGCTTTG CTGG

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 TAGTGCGGCC GCACATTCCT TTGTGTTT

28

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Glu Thr Met His Ala  
1 5 10 15  
Lys Asn

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr  
1 5 10 15  
Lys Lys

35

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